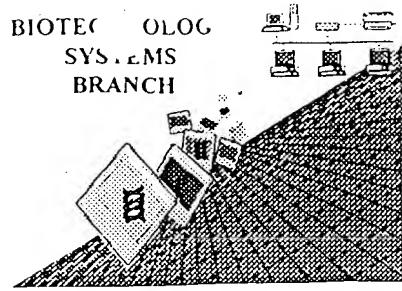


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/654,281

RECEIVED

Source: 1642

MAY 31 2001

Date Processed by STIC: 5-14-01

TECH CENTER 1600 2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

R- Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/654,281

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE.

1	Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	RECEIVED
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	MAY 31 2001 TECH CENTER 1600/290
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6	✓ Variable Length	Sequence(s) <u>1, possibly more</u> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (b) feature section that some may be missing. <u><223></u>	
7	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <u> </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8	Skipped Sequences (OLD RULES)	Sequence(s) <u> </u> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9	Skipped Sequences (NEW RULES)	Sequence(s) <u> </u> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11	✓ Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. <u>Valid response is Artificial Sequence.</u>	
12	Use of <220>Feature (NEW RULES)	Sequence(s) <u> </u> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13	PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001
TIME: 12:18:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

Does Not Comply
Corrected Diskette Needed
pp 1-2, 5

3 <110> APPLICANT: Sedivy, John
4 Kolch, Walter
5 Yeung, Kam Chi
7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation
8 of Cell Proliferation and Growth
10 <130> FILE REFERENCE: 3564/1010
12 <140> CURRENT APPLICATION NUMBER: 09/654,281
13 <141> CURRENT FILING DATE: 2000-09-01
15 <150> PRIOR APPLICATION NUMBER: 60/151,992
16 <151> PRIOR FILING DATE: 1999-09-01
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 42
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial
27 <220> FEATURE:
28 <223> OTHER INFORMATION: consensus sequence
30 <220> FEATURE:
31 <221> NAME/KEY: UNSURE
32 <222> LOCATION: (3)..(5)
33 <223> OTHER INFORMATION: Xaa = any amino acid
36 <220> FEATURE:
37 <221> NAME/KEY: UNSURE
38 <222> LOCATION: (9)..(9)
39 <223> OTHER INFORMATION: a hydrophobic amino acid residue
42 <220> FEATURE:
43 <221> NAME/KEY: UNSURE
44 <222> LOCATION: (11)..(13)
45 <223> OTHER INFORMATION: Xaa = any amino acid
48 <220> FEATURE:
49 <221> NAME/KEY: UNSURE
50 <222> LOCATION: (14)..(14)
51 <223> OTHER INFORMATION: a negatively charged amino acid residue
54 <220> FEATURE:
55 <221> NAME/KEY: UNSURE
56 <222> LOCATION: (15)..(18)
57 <223> OTHER INFORMATION: Xaa = any amino acid residue
60 <220> FEATURE:
61 <221> NAME/KEY: UNSURE
62 <222> LOCATION: (20)..(21)
63 <223> OTHER INFORMATION: Xaa = any amino acid residue
66 <220> FEATURE:
67 <221> NAME/KEY: UNSURE
68 <222> LOCATION: (23)..(23)
69 <223> OTHER INFORMATION: Xaa = 50 of any amino acid residue, 0 to 40 residues may be missi
70 <220> FEATURE:
C--> 71 <223> OTHER INFORMATION: Incomplete <213> response as per section 1.823b of new sequence rules. See #11 on the Error Summary Sheet.
Note: This error is also indicated in sequence #'s 10 and 11. Please review and correct.

Note: This error is also indicated in sequence
ue #s 10 and 11. Please
review and correct.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001
TIME: 12:18:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

73 <220> FEATURE:
74 <221> NAME/KEY: UNSURE
75 <222> LOCATION: (25)...(28)
76 <223> OTHER INFORMATION: Xaa = any amino acid residue
79 <220> FEATURE:
80 <221> NAME/KEY: UNSURE
81 <222> LOCATION: (30)...(30)
82 <223> OTHER INFORMATION: Xaa = 4 of any amino acid residue, 0 to 2 residues may be missing
85 <220> FEATURE:
86 <221> NAME/KEY: UNSURE
87 <222> LOCATION: (32)...(32)
88 <223> OTHER INFORMATION: Xaa = any amino acid residue
91 <220> FEATURE:
92 <221> NAME/KEY: UNSURE
93 <222> LOCATION: (35)...(35)
94 <223> OTHER INFORMATION: Xaa = an aromatic amino acid residue
97 <220> FEATURE:
98 <221> NAME/KEY: UNSURE
99 <222> LOCATION: (37)...(37)
100 <223> OTHER INFORMATION: Xaa = any amino acid residue
103 <220> FEATURE:
104 <221> NAME/KEY: UNSURE
105 <222> LOCATION: (38)...(38)
106 <223> OTHER INFORMATION: a hydrophobic amino acid residue
109 <220> FEATURE:
110 <221> NAME/KEY: UNSURE
111 <222> LOCATION: (39)...(41)
112 <223> OTHER INFORMATION: Xaa = any amino acid residue
115 <400> SEQUENCE: 1
W--> 117 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
118 1 5 10 15
W--> 120 Xaa Xaa Glu Xaa Xaa His (Xaa) Tyr Xaa Xaa Xaa Xaa Pro (Xaa) Gly Xaa
121 20 25 30
W--> 123 His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
124 35 40
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 187
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 2
133 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
134 1 5 10 15
136 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
137 20 25 30
139 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
140 35 40 45
142 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
143 50 55 60
145 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys

"Xaa's" at positions
118, 120, 123 have variable
lengths. Each
23 + 30 only represent
one residue. See
Xaa may be
one residue the error
6 on sheet.
Summary

RAW SEQUENCE LISTING DATE: 05/14/2001
PATENT APPLICATION: US/09/654,281 TIME: 12:18:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

146 65 70 75
 148 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
 149 . 85 90 95
 151 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
 152 . 100 105 110
 154 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
 155 . 115 120 125
 157 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
 158 . 130 135 140
 160 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
 161 145 . 150 155 160
 163 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
 164 . 165 170 175
 166 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 167 . 180 185
 169 <210> SEQ ID NO: 3
 170 <211> LENGTH: 187
 171 <212> TYPE: PRT
 172 <213> ORGANISM: Mus musculus
 174 <220> FEATURE:
 175 <221> NAME/KEY: UNSURE
 176 <222> LOCATION: (150)..(150)
 177 <223> OTHER INFORMATION: Xaa = any amino acid residue
 180 <400> SEQUENCE: 3
 182 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
 183 1 5 10 15
 185 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
 186 . 20 25 30
 188 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
 189 . 35 40 45
 191 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
 192 . 50 55 60
 194 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
 195 65 70 75 80
 197 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
 198 . 85 90 95
 200 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
 201 . 100 105 110
 203 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
 204 . 115 120 125
 206 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
 207 . 130 135 140
 W--> 209 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
 210 145 . 150 155 160
 212 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
 213 . 165 170 175
 215 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 216 . 180 185
 218 <210> SEQ ID NO: 4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001

TIME: 12:18:24

Input Set : A:\ES.txt
 Output Set: N:\CRF3\05142001\I654281.raw

219 <211> LENGTH: 187
 220 <212> TYPE: PRT
 221 <213> ORGANISM: Drosophila
 223 <400> SEQUENCE: 4
 225 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
 226 1 5 10 15
 228 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
 229 20 25 30
 231 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
 232 35 40 45
 234 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
 235 50 55 60
 237 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
 238 65 70 75 80
 240 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
 241 85 90 95
 243 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
 244 100 105 110
 246 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
 247 115 120 125
 249 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
 250 130 135 140
 252 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
 253 145 150 155 160
 255 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
 256 165 170 175
 258 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
 259 180 185
 261 <210> SEQ ID NO: 5
 262 <211> LENGTH: 220
 263 <212> TYPE: PRT
 264 <213> ORGANISM: C. elegans
 266 <400> SEQUENCE: 5
 268 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
 269 1 5 10 15
 271 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
 272 20 25 30
 274 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
 275 35 40 45
 277 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
 278 50 55 60
 280 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
 281 65 70 75 80
 283 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
 284 85 90 95
 286 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
 287 100 105 110
 289 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
 290 115 120 125

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001

TIME: 12:18:24

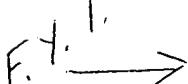
Input Set : A:\ES.txt

Output Set: N:\CRF3\05142001\I654281.raw

292 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
 293 130 135 140
 295 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln
 296 145 150 155 160
 298 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
 299 165 170 175
 301 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
 302 180 185 190
 304 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
 305 195 200 205
 307 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
 308 210 215 220
 310 <210> SEQ ID NO: 6
 311 <211> LENGTH: 181
 312 <212> TYPE: PRT
 313 <213> ORGANISM: Antirrhinum-CEN
 315 <400> SEQUENCE: 6
 317 Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
 318 1 5 10 15
 320 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
 321 20 25 30
 323 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
 324 35 40 45
 326 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
 327 50 55 60
 329 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
 330 65 70 75 80
 332 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
 333 85 90 95
 335 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
 336 100 105 110
 338 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
 339 115 120 125
 341 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
 342 130 135 140
 344 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
 345 145 150 155 160
 347 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
 348 165 170 175
 350 Ala Ala Arg Arg Arg
 351 180
 353 <210> SEQ ID NO: 7
 354 <211> LENGTH: 176
 355 <212> TYPE: PRT
 356 <213> ORGANISM: Aradopsis-TFL1
 358 <400> SEQUENCE: 7
 360 Met Glu Asn Met Gly Thr Arg Val Ile Glu Pro Leu Ile Met Gly Arg
 361 1 5 10 15
 363 Val Val Gly Asp Val Leu Asp Phe Phe Thr Pro Thr Lys Met Asn

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001

TIME: 12:18:25

Input Set : A:\ES.txt

Output Set: N:\CRF3\05142001\I654281.raw

L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:460 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:480 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11